

Prof Jacques Theron

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Orbiviruses

Jacques Theron graduated with a PhD degree from the University of Pretoria in 1996. Whilst completing his PhD, he was appointed as lecturer in the Department of Microbiology and Plant Pathology, and currently holds the position of professor. He is the author of 42 peer-reviewed publications and has been invited to co-author eight book chapters. He is also co-inventor of two patents concerning detection of selected bacterial pathogens in water sources. His research findings have formed the basis of 131 contributions at conferences, comprising 85 contributions at national conferences and 46 at international conferences. In recognition of his research

he received the Water Institute of Southern Africa (WISA) bi-annual award for most promising young researcher in 2000 and an Exceptional Young Researcher award from the University of Pretoria in 2002.

Research

African horse sickness, of which African horse sickness virus (AHSV) is the aetiological agent, is the most devastating and rapidly fatal disease amongst horses. Although the veterinary and vaccine-related

Key Publications

Stassen, L., Huismans, H. & Theron, J. 2007. Silencing of African horse sickness virus VP7 protein expression in cultured cells by RNA interference. *Virus Genes* 35: 777-783.

Stassen, L., Huismans, H. & Theron, J. 2011. Membrane permeabilization of the African horse sickness virus VP5 protein is mediated by two N-terminal amphipathic a-helices. *Archives of Virology* 156: 711-715.

Stassen, L., Huismans, H. & Theron, J. 2012. African horse sickness virus induces apoptosis in cultured mammalian cells. *Virus Res.* 163: 385-389.



aspects of AHSV have received some attention, AHSV replication and the role of individual viral proteins in this process – as well as AHSV-host cell interactions – are very much unexplored. Prof Theron's immediate research focus is on AHSV structural and non-structural proteins, whose roles in viral processes such as cell entry and production of viable progeny virions remain undefined. To this end, they have established a RNA interference (RNAi) platform for analysis of virus gene function, and developed a single-gene replacement reverse genetic approach to enable introduction of defined mutations into the viral genome. The data generated should not only contribute substantially to unravelling the molecular mechanisms underlying AHSV propagation, virulence and pathogenicity, but may also find application in aiding the design of alternative control strategies through intervention of its normal replication cycle.